List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mining germplasm panels and phenotypic datasets to identify loci for resistance to Phytophthora sojae in soybean. Plant Genome, 2021, 14, e20063.	2.8	13
2	Identification of Quantitative Disease Resistance Loci Toward Four Pythium Species in Soybean. Frontiers in Plant Science, 2021, 12, 644746.	3.6	7
3	Network Inference of Transcriptional Regulation in Germinating Low Phytic Acid Soybean Seeds. Frontiers in Plant Science, 2021, 12, 708286.	3.6	1
4	Genetic interactions regulating seed phytate and oligosaccharides in soybean (Glycine maxÂL.). PLoS ONE, 2020, 15, e0235120.	2.5	8
5	A transcriptional regulatory network of Rsv3-mediated extreme resistance against Soybean mosaic virus. PLoS ONE, 2020, 15, e0231658.	2.5	8
6	<i>Soybean mosaic virus</i> : a successful potyvirus with a wide distribution but restricted natural host range. Molecular Plant Pathology, 2018, 19, 1563-1579.	4.2	67
7	Inference of Transcription Regulatory Network in Low Phytic Acid Soybean Seeds. Frontiers in Plant Science, 2017, 8, 2029.	3.6	16
8	A Method for Combining Isolates of Phytophthora sojae to Screen for Novel Sources of Resistance to Phytophthora Stem and Root Rot in Soybean. Plant Disease, 2016, 100, 1424-1428.	1.4	12
9	Candidate Gene Sequence Analyses toward Identifying Rsv3 â€Type Resistance to Soybean Mosaic Virus. Plant Genome, 2016, 9, plantgenome2015.09.0088.	2.8	18
10	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. Theoretical and Applied Genetics, 2016, 129, 453-468.	3.6	37
11	Genome-wide transcriptome analyses of developing seeds from low and normal phytic acid soybean lines. BMC Genomics, 2015, 16, 1074.	2.8	18
12	Genetic variants in root architecture-related genes in a Glycine soja accession, a potential resource to improve cultivated soybean. BMC Genomics, 2015, 16, 132.	2.8	67
13	Metabolite Profiling of Soybean Seed Extracts from Near-Isogenic Low and Normal Phytate Lines Using Orthogonal Separation Strategies. Journal of Agricultural and Food Chemistry, 2015, 63, 9879-9887.	5.2	11
14	Mapping Net Blotch Resistance in â€~Nomini' and Clho 2291 Barley. Crop Science, 2014, 54, 2596-2602.	1.8	23
15	Physiological and transcriptomic characterization of submergence and reoxygenation responses in soybean seedlings. Plant, Cell and Environment, 2014, 37, 2350-2365.	5.7	86
16	The HC-Pro and P3 Cistrons of an Avirulent <i>Soybean mosaic virus</i> Are Recognized by Different Resistance Genes at the Complex <i>Rsv1</i> Locus. Molecular Plant-Microbe Interactions, 2013, 26, 203-215.	2.6	63
17	Evolution of a Complex Disease Resistance Gene Cluster in Diploid <i>Phaseolus</i> and Tetraploid <i>Glycine</i> Â Â Â. Plant Physiology, 2012, 159, 336-354.	4.8	76
18	Registration of Fusarium Head Blight–Resistant Soft Red Winter Wheat Germplasm VA04Wâ€433 and VA04Wâ€474. Journal of Plant Registrations, 2012, 6, 111-116.	0.5	7

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19	Amino acid changes in P3, and not the overlapping <i>pipo</i> â€encoded protein, determine virulence of <i>Soybean mosaic virus</i> on functionally immune <i>Rsv1</i> â€genotype soybean. Molecular Plant Pathology, 2011, 12, 799-807.	4.2	56
20	Experimental Adaptation of an RNA Virus Mimics Natural Evolution. Journal of Virology, 2011, 85, 2557-2564.	3.4	33
21	Fine Mapping and Candidate Gene Discovery of the Soybean Mosaic Virus Resistance Gene, <i>Rsv4</i> . Plant Genome, 2010, 3, .	2.8	69
22	Mapping Quantitative Trait Loci for Partial Resistance to <i>Phytophthora sojae</i> in a Soybean Interspecific Cross. Crop Science, 2010, 50, 628-635.	1.8	53
23	Identification of Candidate Gene Mutation Associated With Low Stachyose Phenotype in Soybean Line PI200508. Crop Science, 2009, 49, 247-255.	1.8	43
24	Genetic Basis of the Lowâ€₽hytate Trait in the Soybean Line CX1834. Crop Science, 2009, 49, 69-76.	1.8	53
25	Validation and Interaction of the <i>Soybean Mosaic Virus</i> Lethal Necrosis Allele, <i>Rsv1â€n</i> , in PI 507389. Crop Science, 2009, 49, 1277-1283.	1.8	10
26	Infection and genotype remodel the entire soybean transcriptome. BMC Genomics, 2009, 10, 49.	2.8	50
27	Marker-assisted identification of resistance genes to soybean mosaic virus in soybean lines. Euphytica, 2009, 169, 375-385.	1.2	16
28	Spatial and temporal patterns of associations between quantitative characters and resistance to scald in barley. Hereditas, 2008, 115, 1-8.	1.4	0
29	Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean Â. Plant Physiology, 2008, 148, 1740-1759.	4.8	140
30	Replication of Nonautonomous Retroelements in Soybean Appears to Be Both Recent and Common Â. Plant Physiology, 2008, 148, 1760-1771.	4.8	57
31	Pyramiding of Soybean Mosaic Virus Resistance Genes by Markerâ€Assisted Selection. Crop Science, 2008, 48, 517-526.	1.8	96
32	Validation of Lowâ€Phytate QTLs and Evaluation of Seedling Emergence of Lowâ€Phytate Soybeans. Crop Science, 2008, 48, 1355-1364.	1.8	21
33	A Modified Colorimetric Method for Phytic Acid Analysis in Soybean. Crop Science, 2007, 47, 1797-1803.	1.8	182
34	Validating molecular markers for barley leaf rust resistance genes Rph5 and Rph7. Plant Breeding, 2007, 126, 458-463.	1.9	15
35	Confirmation of Three Quantitative Trait Loci Conferring Adult Plant Resistance to Powdery Mildew in Two Winter Wheat Populations. Euphytica, 2007, 155, 1-13.	1.2	55
36	Interrelationships among Agronomic and Seed Quality Traits in an Interspecific Soybean Recombinant Inbred Population. Crop Science, 2006, 46, 1253-1259.	1.8	45

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37	Application of comparative genomics in developing molecular markers tightly linked to the virus resistance gene Rsv4 in soybean. Genome, 2006, 49, 380-388.	2.0	54
38	Cloning, genetic and physical mapping of resistance gene analogs in barley (Hordeum vulgare L.). Plant Breeding, 2006, 125, 32-42.	1.9	8
39	Validation of two major quantitative trait loci for fusarium head blight resistance in Chinese wheat line W14. Plant Breeding, 2006, 125, 99-101.	1.9	99
40	Potential for effective marker-assisted selection of three quantitative trait loci conferring adult plant resistance to powdery mildew in elite wheat breeding populations. Plant Breeding, 2006, 125, 430-436.	1.9	18
41	High-resolution mapping of the barley leaf rust resistance gene Rph5 using barley expressed sequence tags (ESTs) and synteny with rice. Theoretical and Applied Genetics, 2005, 111, 1651-1660.	3.6	23
42	Recombination Within a Nucleotide-Binding-Site/Leucine-Rich-Repeat Gene Cluster Produces New Variants Conditioning Resistance to Soybean Mosaic Virus in Soybeans. Genetics, 2004, 166, 493-503.	2.9	139
43	Detection and genotyping of SNPs tightly linked to two disease resistance loci, Rsv1 and Rsv3, of soybean. Plant Breeding, 2004, 123, 305-310.	1.9	74
44	A Diagnostic Analysis of Genetic Differentiation Among Subpopulations of a Barley Composite Cross Using Isozyme Markers. Hereditas, 2004, 118, 63-70.	1.4	2
45	RFLPs in Cultivated Barley and Their Application in the Evaluation of Malting Quality Cultivars. Hereditas, 2004, 121, 21-29.	1.4	8
46	Molecular Mapping of Leaf Rust Resistance Gene <i>Rph</i> 5 in Barley. Crop Science, 2003, 43, 388-393.	1.8	18
47	Molecular Mapping of Leaf Rust Resistance Gene 5 in Barley. Crop Science, 2003, 43, 388.	1.8	15
48	Genetic and Sequence Analysis of Markers Tightly Linked to the <i>Soybean mosaic virus</i> Resistance Gene, <i>Rsv</i> 3. Crop Science, 2002, 42, 265-270.	1.8	99
49	Genetic and Sequence Analysis of Markers Tightly Linked to the Resistance Gene, 3. Crop Science, 2002, 42, 265.	1.8	47
50	Genetic and Sequence Analysis of Markers Tightly Linked to the Soybean mosaic virus Resistance Gene, Rsv3. Crop Science, 2002, 42, 265-270.	1.8	59
51	Identification of Molecular Markers Associated with Adult Plant Resistance to Powdery Mildew in Common Wheat Cultivar Massey. Crop Science, 2001, 41, 1268-1275.	1.8	106
52	Diversity and evolution of a non-TIR-NBS sequence family that clusters to a chromosomal ''hotspot― for disease resistance genes in soybean. Theoretical and Applied Genetics, 2001, 103, 406-414.	3.6	39
53	Identification of quantitative trait loci controlling sucrose content in soybean (Glycine max). Molecular Breeding, 2000, 6, 105-111.	2.1	77
54	Targeted resistance gene mapping in soybean using modified AFLPs. Theoretical and Applied Genetics, 2000, 100, 1279-1283.	3.6	62

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55	Expression of two soybean resistance gene candidates shows divergence of paralogous single-copy genes. Theoretical and Applied Genetics, 2000, 101, 789-795.	3.6	19
56	Molecular Marker Mapping of <i>RSV</i> 4, a Gene Conferring Resistance to all Known Strains of Soybean Mosaic Virus. Crop Science, 2000, 40, 1434-1437.	1.8	139
57	Patterns of cytosine methylation in an elite rice hybrid and its parental lines, detected by a methylation-sensitive amplification polymorphism technique. Molecular Genetics and Genomics, 1999, 261, 439-446.	2.4	456
58	Title is missing!. Molecular Breeding, 1998, 4, 129-136.	2.1	54
59	Epistasis plays an important role as genetic basis of heterosis in rice. Science in China Series C: Life Sciences, 1998, 41, 293-302.	1.3	6
60	Rpg1, a soybean gene effective against races of bacterial blight, maps to a cluster of previously identified disease resistance genes. Theoretical and Applied Genetics, 1998, 96, 1013-1021.	3.6	80
61	Molecular Mapping, Chromosomal Assignment, and Genetic Diversity Analysis of Phytochrome Loci in Barley (Hordeum vulgare). Journal of Heredity, 1997, 88, 21-26.	2.4	13
62	Importance of epistasis as the genetic basis of heterosis in an elite rice hybrid. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 9226-9231.	7.1	660
63	Correlation between Molecular Marker Distance and Hybrid Performance in U.S. Southern Long Grain Rice. Crop Science, 1997, 37, 145-150.	1.8	61
64	Copia-like retrotransposons in rice: sequence heterogeneity, species distribution and chromosomal locations. Plant Molecular Biology, 1997, 33, 1051-1058.	3.9	27
65	Molecularmarker diversity and hybrid sterility in indica-japonica rice crosses. Theoretical and Applied Genetics, 1997, 95, 112-118.	3.6	66
66	Extraordinarily polymorphic ribosomal DNA in wild and cultivated rice. Genome, 1996, 39, 1109-1116.	2.0	22
67	Regions of the Genome that Affect Agronomic Performance in Twoâ€Row Barley. Crop Science, 1996, 36, 1053-1062.	1.8	191
68	Isolation of a superfamily of candidate disease-resistance genes in soybean based on a conserved nucleotide-binding site Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 11751-11756.	7.1	332
69	Identification of quantitative trait loci controlling resistance to gray leaf spot disease in maize. Theoretical and Applied Genetics, 1996, 93, 539-546.	3.6	86
70	Molecular-marker analysis of seed-weight: genomic locations, gene action, and evidence for orthologous evolution among three legume species. Theoretical and Applied Genetics, 1996, 93, 574-579.	3.6	134
71	An analysis of hybrid sterility in rice using a diallel cross of 21 parents involving indica, japonica and wide compatibility varieties. Euphytica, 1996, 90, 275-280.	1.2	68
72	Divergence and allelomorphic relationship of a soybean virus resistance gene based on tightly linked DNA microsatellite and RFLP markers. Theoretical and Applied Genetics, 1996, 92, 64-69.	3.6	30

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73	Amplified fragment length polymorphism (AFLP) in soybean: species diversity, inheritance, and near-isogenic line analysis. Theoretical and Applied Genetics, 1996, 93, 392-401.	3.6	234
74	Molecular marker heterozygosity and hybrid performance in indica and japonica rice. Theoretical and Applied Genetics, 1996, 93, 1218-1224.	3.6	96
75	Development of simple sequence repeat DNA markers and their integration into a barley linkage map. Theoretical and Applied Genetics, 1996, 93-93, 869-876.	3.6	323
76	Analysis of the barley and rice genomes by comparative RFLP linkage mapping. Theoretical and Applied Genetics, 1996, 92, 541-551.	3.6	90
77	Analysis of the barley and rice genomes by comparative RFLP linkage mapping. Theoretical and Applied Genetics, 1996, 92, 541-551.	3.6	22
78	Amplified fragment length polymorphism (AFLP) in soybean: species diversity,inheritance, and near-isogenic line analysis. Theoretical and Applied Genetics, 1996, 93, 392-401.	3.6	45
79	Identification of quantitative trait loci controlling resistance to gray leaf spot disease in maize. Theoretical and Applied Genetics, 1996, 93, 539-546.	3.6	8
80	Molecular divergence and hybrid performance in rice. Molecular Breeding, 1995, 1, 133-142.	2.1	85
81	Comparison of restriction fragment length polymorphisms in wild and cultivated barley. Genome, 1995, 38, 298-306.	2.0	34
82	Microsatellite and amplified sequence length polymorphisms in cultivated and wild soybean. Genome, 1995, 38, 715-723.	2.0	128
83	Construction of a sorghum RFLP linkage map using sorghum and maize DNA probes. Genome, 1994, 37, 590-594.	2.0	38
84	Molecular marker analyses of powdery mildew resistance in barley. Theoretical and Applied Genetics, 1994, 88, 733-740.	3.6	32
85	A diallel analysis of heterosis in elite hybrid rice based on RFLPs and microsatellites. Theoretical and Applied Genetics, 1994, 89-89, 185-192.	3.6	139
86	Comparative analysis of microsatellite DNA polymorphism in landraces and cultivars of rice. Molecular Genetics and Genomics, 1994, 245, 187-194.	2.4	198
87	Using bulked extremes and recessive class to map genes for photoperiod-sensitive genic male sterility in rice Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 8675-8679.	7.1	248
88	Extraordinarily polymorphic microsatellite DNA in barley: species diversity, chromosomal locations, and population dynamics Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 5466-5470.	7.1	558
89	RFLP Markers Linked to the Durable Stem Rust Resistance GeneRpg1in Barley. Molecular Plant-Microbe Interactions, 1994, 7, 298.	2.6	25
90	RFLP and Microsatellite Mapping of a Gene for Soybean Mosaic Virus Resistance. Phytopathology, 1994, 84, 60.	2.2	188

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91	A molecular, isozyme and morphological map of the barley (Hordeum vulgare) genome. Theoretical and Applied Genetics, 1993, 86, 705-712.	3.6	652
92	lsozyme variation within and among populations of Rhynchosporium secalis in Europe, Australia and the United States. Mycological Research, 1993, 97, 49-58.	2.5	82
93	Patterns of Restriction Fragment Length Polymorphisms in Corn, Barley and Rice. Current Plant Science and Biotechnology in Agriculture, 1993, , 254-257.	0.0	0
94	Ribosomal DNA polymorphisms and the Oriental-Occidental genetic differentiation in cultivated barley. Theoretical and Applied Genetics, 1992, 84-84, 682-687.	3.6	28
95	Genetic diversity and differentiation of indica and japonica rice detected by RFLP analysis. Theoretical and Applied Genetics, 1992, 83, 495-499.	3.6	228
96	Use of RFLP markers to search for alleles in a maize population for improvement of an elite hybrid. Theoretical and Applied Genetics, 1992, 83-83, 903-911.	3.6	37
97	Interrelationships of allozymes and ribosomal DNA alleles in wild barley. Euphytica, 1992, 61, 113-122.	1.2	0
98	Molecular Marker Information and Selection of Parents in Corn Breeding Programs. Crop Science, 1992, 32, 301-304.	1.8	34
99	Molecular Markers and Grouping of Parents in Maize Breeding Programs. Crop Science, 1991, 31, 718-723.	1.8	138
100	Effects on adaptedness of variations in ribosomal DNA copy number in populations of wild barley (Hordeum vulgare ssp. spontaneum) Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 8741-8745.	7.1	47
101	Worldwide pattern of multilocus structure in barley determined by discrete log-linear multivariate analyses. Theoretical and Applied Genetics, 1990, 80, 121-128.	3.6	26
102	Genetic diversity and ecogeographical differentiation among ribosomal DNA alleles in wild and cultivated barley Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 8486-8490.	7.1	82
103	Genetic and molecular organization of ribosomal DNA (rDNA) variants in wild and cultivated barley Genetics, 1990, 126, 743-751.	2.9	40
104	Influence of environments on the development of multivariate structures in a barley composite cross at three locations. Genome, 1989, 32, 40-45.	2.0	3
105	Chloroplast DNA polymorphisms in lodgepole and jack pines and their hybrids Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 2097-2100.	7.1	409
106	Ribosomal DNA spacer-length polymorphisms in barley: mendelian inheritance, chromosomal location, and population dynamics Proceedings of the National Academy of Sciences of the United States of America, 1984, 81, 8014-8018.	7.1	4,434
107	Evolution of resistance to scald, powdery mildew, and net blotch in barley composite cross II populations. Theoretical and Applied Genetics, 1983, 66-66, 279-283.	3.6	21